

AMENDMENTS TO THE CLAIMS

1-19. (Canceled)

20. (Original) A tree breeding method comprising:

- (a) mixing pollen obtained from a breeding group comprising a plurality of parental trees to obtain a pollen polymix;
- (b) pollinating female reproductive structures from each parental tree in the plurality of parental trees with the pollen polymix to obtain a plurality of progeny lots, wherein each progeny lot comprises seeds obtained from a different cross between the pollen polymix and each different parental tree of the plurality of parental trees;
- (c) evaluating progeny trees grown from each of the progeny lots using objective criteria to obtain a phenotype score;
- (d) determining the pedigree of a plurality of progeny trees using DNA analysis; and
- (e) using the pedigree and phenotype score to identify elite trees for use in a next generation of tree breeding.

21. (Previously presented) The method of Claim 20 additionally comprising selecting candidate trees from within the progeny trees based upon their phenotype score, wherein step (d) is performed on the candidate trees, and step (e) is performed using the pedigree and phenotype scores from the candidate trees to identify elite trees for use in a next generation of plant breeding.

22. (Previously presented) The method of Claim 20, wherein the pedigree and phenotype scores are used to estimate the breeding values of a plurality of progeny and parental trees, and the breeding values are used to identify the elite trees for use in a next generation of breeding.

23. (Previously presented) The method of Claim 22, wherein the elite plants are derived from parental plants that have a high general combining ability.

24. (Previously presented) The method of Claim 20, wherein the pedigree determined is paternity.

25. (Previously presented) The method of Claim 20, wherein the pedigree determined is paternity and maternity.

26. (Previously presented) The method of Claim 20, wherein the phenotype score is obtained for a phenotype selected from the group consisting of disease resistance, growth rate, growth habit, chemical composition of any plant tissue, drought resistance, temperature hardiness, elevation adaptation, fecundity, and any combination thereof.

27. (Currently amended) The method of Claim 20, wherein the DNA analysis is performed using a DNA analysis method selected from the group consisting of DNA sequencing, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide repeat microsatellites (~~i.e., simple sequence repeats (SSR)~~), di-, tri-, and tetra-nucleotide repeat SSRs, SSR-anchored PCR, sequenced tagged sites (STS), single nucleotide polymorphism (SNP), single stranded conformational polymorphism (SSCP), sequenced characterized amplified regions (SCAR), allele-specific associated primers (ASAP), single primer amplification reaction (SPARs), and cleaved amplified polymorphic sequences (CAP).

28. (Previously presented) The method of Claim 20, wherein a plurality of pollen polymixes are prepared, each pollen polymix comprised of pollen obtained from a plurality of different parental trees, each pollen polymix of the plurality of pollen polymixes being used to pollinate female reproductive structures from parental trees whose pollen or that of its close relatives are not represented in the pollinating pollen polymix.

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29. (New) The method of Claim 27, wherein the DNA analysis method is performed using single nucleotide repeat microsatellite analysis.

30. (New) The method of Claim 20, wherein the breeding group consists of conifer species.

31. (New) The method of Claim 30, wherein the DNA analysis method is performed using single nucleotide repeat microsatellite analysis.

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